

orf-24 SEQ ID NO:99	34088- 39613	Polyketide synthase ( <i>blmVIII</i> )	Gapped-blast comparison <sup>1</sup>	F: ATGAGCCATGCCGACGCG R: TCACAGCACCACCTCTTC	37 38
orf-25 SEQ ID NO:98	30891- 34091	Peptide synthetase (NRPS-7, <i>blmIX</i> )	Gapped-blast comparison <sup>1</sup>	F: ATGACCCCGGCCGCCGAC R: TCATCGTCCGCCGCCTTT	39 40
orf-26 SEQ ID NO:97	24406- 30894	Peptide synthetase (NRPS-9-8, <i>blmX</i> )	Gapped-blast comparison <sup>1</sup>	F: ATGCCTCGGTGTGCCCGA R: TCATTCCGGCGGCACCTCC	41 42
orf-27 SEQ ID NO:96	22127- 24193	Peptide synthetase (condensation, <i>blmXI</i> )	Gapped-blast comparison <sup>1</sup>	F: GTGGGTTTCCGTCGAGCG R: TTACACCCTCCGTTTCTC	43 44
orf-28 SEQ ID NO:95	21367- 22086	Phosphatidylserine decarboxylase	Gapped-blast comparison <sup>1</sup>	F: ATGGCACAGGACCTGAAC R: TCAACGCCACCGGATCTT	45 46
orf-29 SEQ ID NO:94	19161- 20909	Transmembrane transporter	Gapped-blast comparison <sup>1</sup>	F: GTGAGCTCCCTCGCCGTC R: TCATCGTCCGGCACTCGG	47 48
orf-30 SEQ ID NO:93	18823- 19164	Metal dependent regulatory element	Gapped-blast comparison <sup>1</sup>	F: GTGCCGGTTCGCTGTAT R: TCACCGGGCACTGACCTC	49 50
orf-31 SEQ ID NO:116	18660- 18307	PHNA homolog	Gapped-blast comparison <sup>1</sup>	F: GTGACCGAGAACCTTCCG R: TCAGACCTTCTTGACCAC	51 52
orf-32 SEQ ID NO:117	17736- 9211	Peptide synthetase (NRPS-11-10)	Gapped-blast comparison <sup>1</sup>	F: ATGGCCTCAGACGCTTTG R: TCATTGAGACTCCTCCTC	53 54
orf-33 SEQ ID NO:118	9214- 7859	Putative transporter	Gapped-blast comparison <sup>1</sup>	F: ATGATGAAGTCAAGCCGC R: TCAGTGGCTTACAAGGAG	55 56
orf-34 SEQ ID NO:119	7797- 6784	Homolog of clavaminic acid synthase	Gapped-blast comparison <sup>1</sup>	F: ATGACTGACCTGCCGTTG R: TCACACCAGCAGCGAGGT	57 58
orf-35 SEQ ID NO:120	6773- 6021	Thioesterase	Gapped-blast comparison <sup>1</sup>	F: ATGGATTTCCCCCTCACC R: TCATGCCCTACCTCGGC	59 60
orf-36 SEQ ID NO:121	6024- 4741	Putative transporter	Gapped-blast comparison <sup>1</sup>	F: ATGACCGCGCGCTCGAC R: TCACTCCTCGGCTTCGGC	61 62
orf-37 SEQ ID NO:122	4733- 3915	Unknown	Gapped-blast comparison <sup>1</sup>	F: GTGTCCAAGAACGCGGCG R: TCATCGGCTCGCCTCGTG	63 64
orf-38 SEQ ID NO:123	3918- 2182	Peptide synthetase (NRPS-12)	Gapped-blast comparison <sup>1</sup>	F: ATGACCCTCACCTGCGG R: TCACTCGGGCACTCCTTC	65 66
orf-39 SEQ ID NO:124	2185- 1199	Regulatory gene (homolog of <i>SyrP</i> )	Gapped-blast comparison <sup>1</sup>	F: GTGACCGTTCCGTAACG R: TCATGAGTCCGCCGAGGT	67 68
orf-40 SEQ ID NO:125	1015-1	Peptide synthetase	Gapped-blast comparison <sup>1</sup>	F: ATGACAGAGGTCCGAGGT R: CCCGGCAACCGCCCTCCC	69 70
orf-41 SEQ ID NO:126	On a separate sequence	4'-phosphopantetheinyl transferase ( <i>pptA</i> )	Expression and biochemical characterization. <sup>2</sup>	F: GTGATCGCCGCCCTCCTG R: TTACGGGACGGCGTCCG	71 72

In accordance with 37 CFR §1.121 a marked up version of the above-amended paragraph(s) illustrating the changes introduced by the forgoing amendment(s) are provided in Appendix A.

#### In the Claims:

Please amend the claims by substituting the following claims for the corresponding previously pending claims of the same number(s):